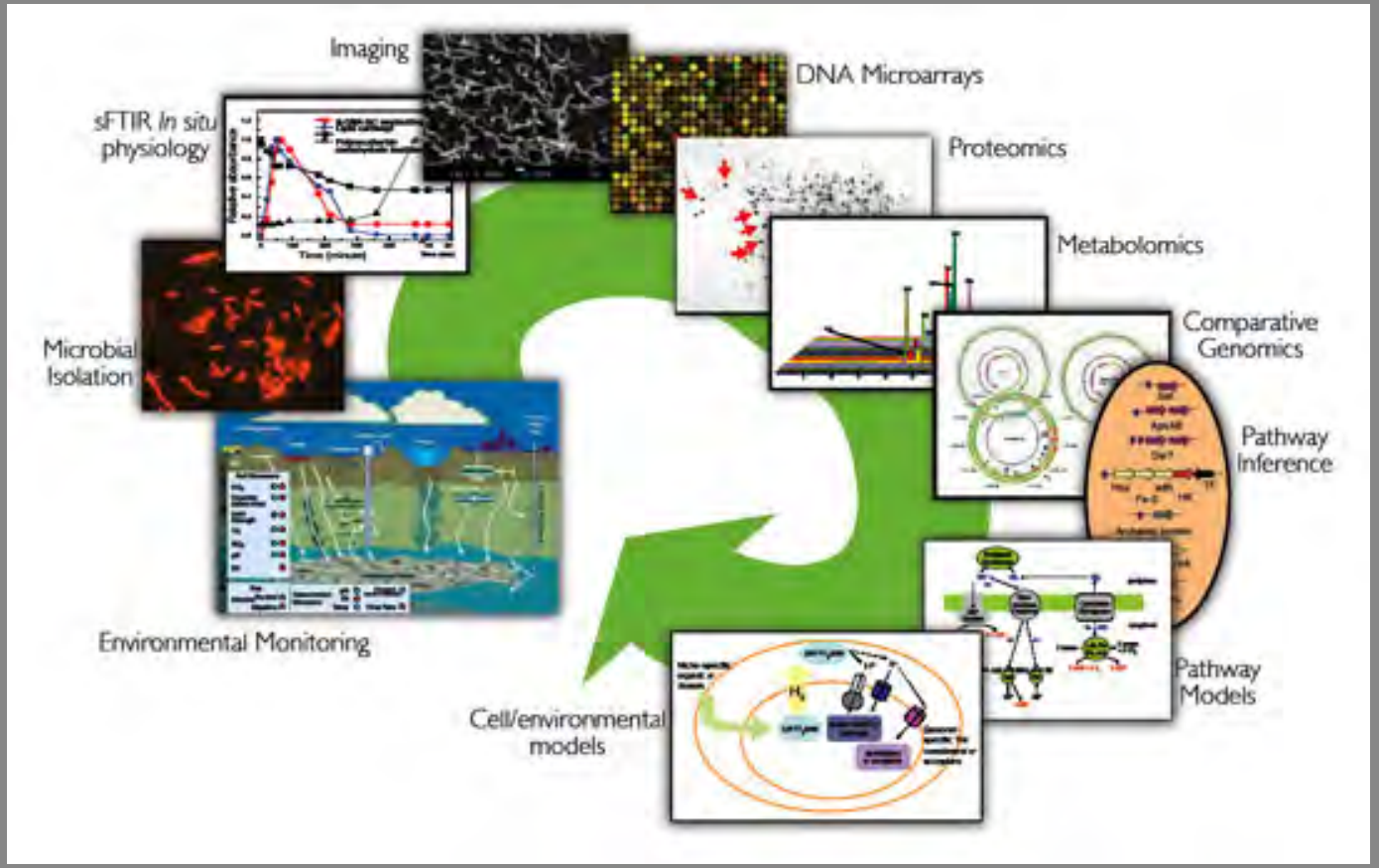
Information Dashboards

http://vimss.lbl.gov

- Dashboard Design
- Team Science Approach
- Project Milestones &
- WBS & Budgets
- Working Dashboards



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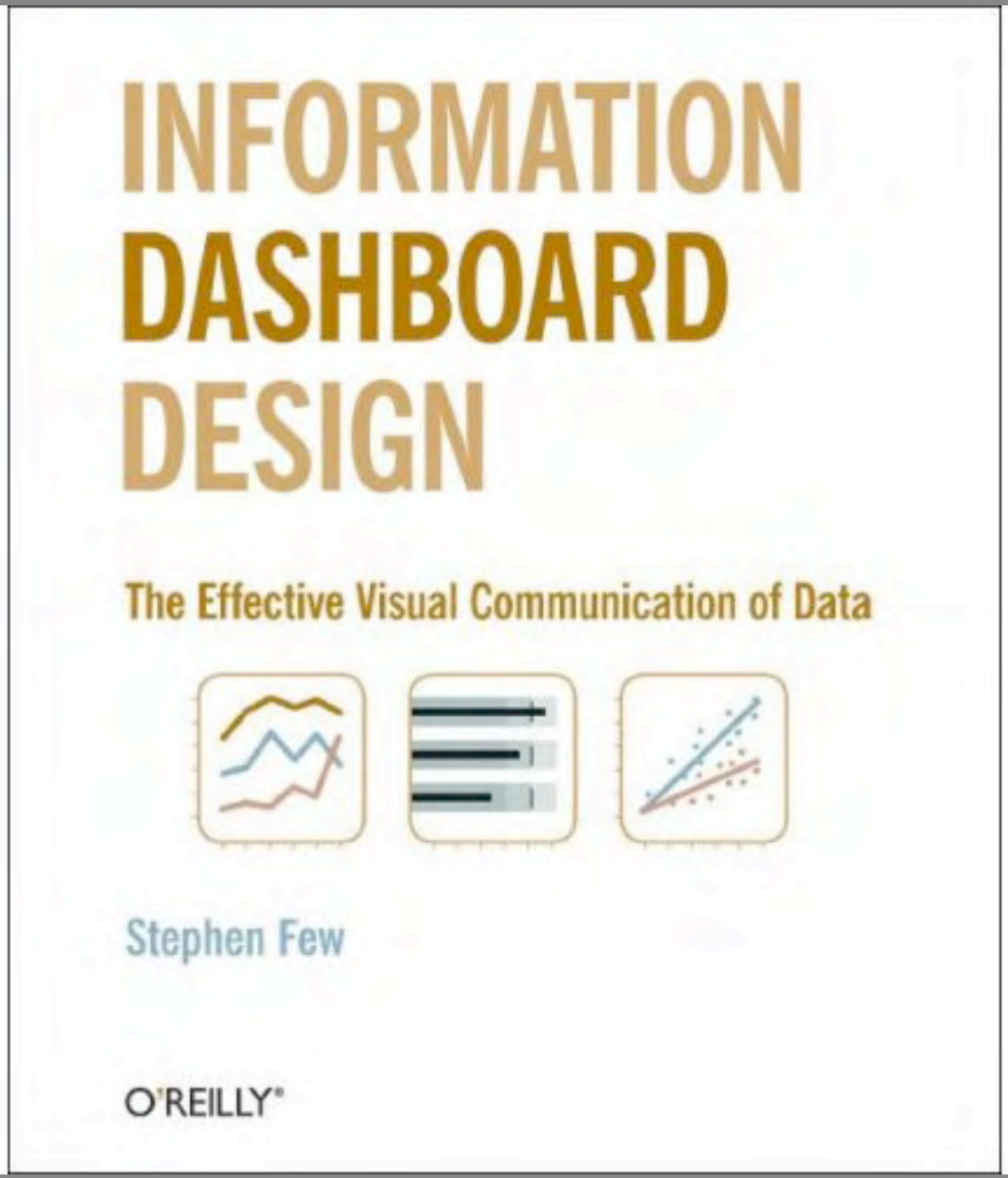
Physical Biosciences Division

ACKNOWLEDGEMENT

ESPP2 is part of the Virtual Institute for Microbial Stress and Survival supported by the U. S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomics Program:GTL through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U. S. Department of Energy.

Information Dashboard Design: The Effective Visual Communication of Data



About the Author

Stephen Few has worked for over 20 years as an IT innovator, consultant, and teacher. Today, as Principal of the consultancy Perceptual Edge, Stephen focuses on data visualization for analyzing and communicating quantitative business information. He teaches in the MBA program at the University of California, Berkeley. You can learn more about Stephen's work and access an entire library of articles at www.perceptualedge.com.

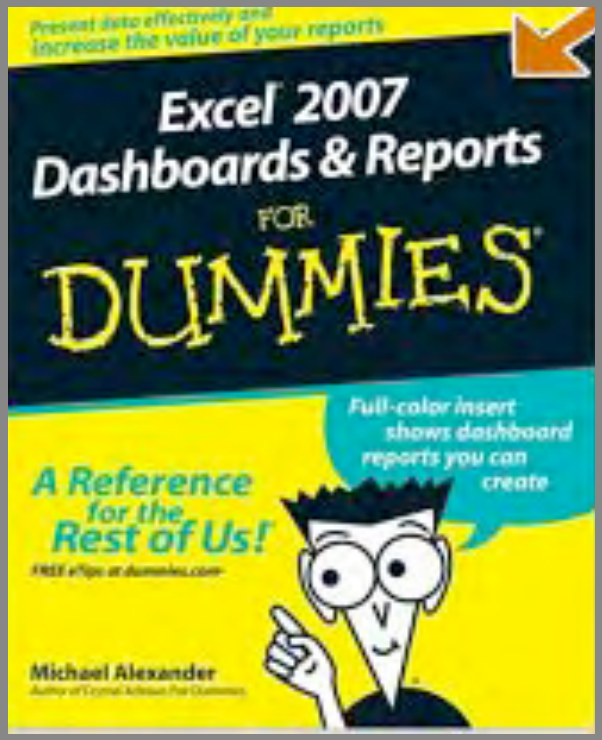
Dashboards - defined

"A dashboard is a visual interface that provides at-a-glance views into key measures relevant to a particular objective or business process."

Key Attributes:

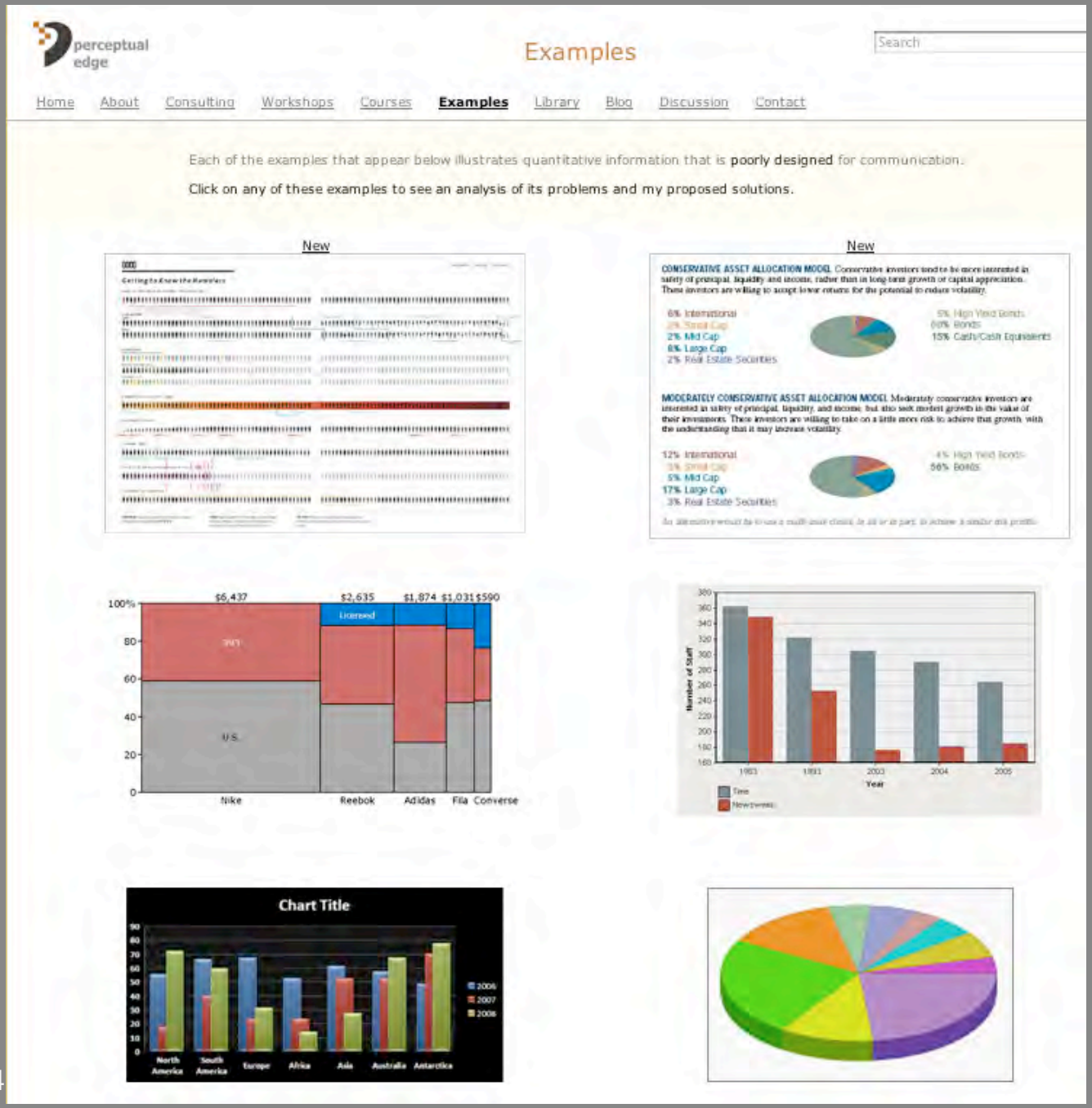
- ✓ Graphical to focus attention on key trends, comparisons and exceptions
- ✓ Display only relevant data
- ✓ Inherently contain predefined conclusions

Note: Collecting user requirements is KEY



from 'Excel 2007 Dashboards & Reports for Dummies' by Michael Alexander

Dashboards - bad examples



Common Problems:

Positioning content in places that don't fit its importance

Positioning content in places that fail to support its use

Including items that serve no useful purpose

Sizing content larger than it deserves

Separating content excessively

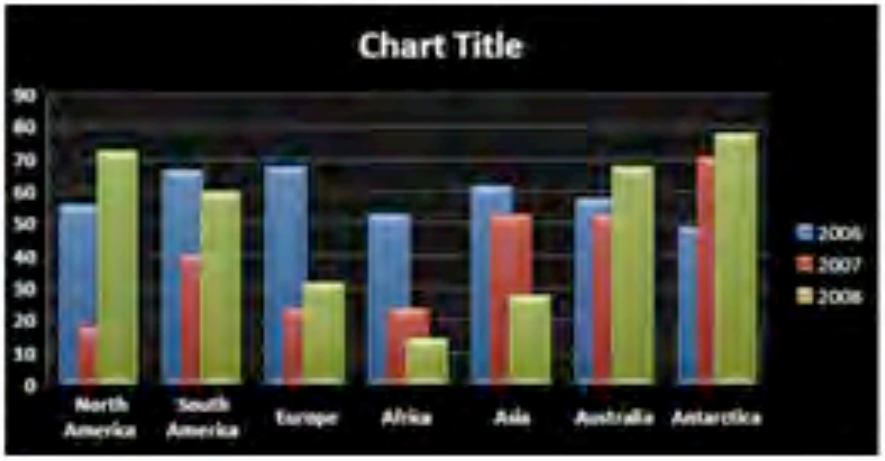
Visually featuring content & other items more than they deserve

Failing to link contents & other items that are related

Visually suggesting links between unrelated content

Enforcing a rigid symmetrical grid

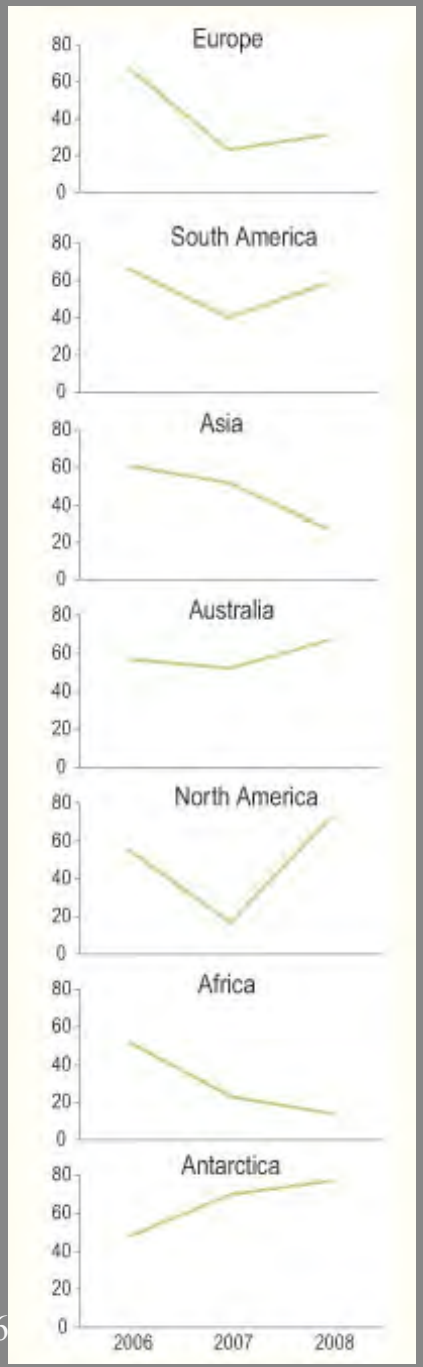
Dashboards - bad examples



Here are a few of this graph's problems:

- There are several distracting (and detracting) visual effects: the reflection of light, transparency, and 3-D effects on the bars (and squares in the legend) add no value.
- The bars have been overlayed on one another, which partially obscures the first two sets and gives them different visual salience. Because the bars for the year 2008 appear in the forefront of each cluster, their greater importance is implied, which was probably not intended. While I can't be sure, the graph's original post date of 2005, suggests that these values are projections, albeit unbelievably volatile ones. Without knowing more about the data, I can't say for sure, but the 2006 projections are probably the surest and most relevant, yet they are partly obscured by the other two years.
- Although the gridlines in this graph are thin and light, because these values are projections, we probably don't need to know precise values. As such, the gridlines are not necessary.
- The bar colors are more intense than they should be. The use of high-intensity colors should be reserved for making important data salient. Regular data should be shown using less intense colors. After all, when you display all of your data to stand out, nothing does.
- The continents have not been ordered in a logical way. At the very least they could have been alphabetized, but, as we'll see below, there's almost always a better way to order your data.
- Although bar graphs are great for showing and comparing the magnitudes of different variables, they are inferior to lines for showing how the values change through time. Because the pattern of change through time is likely more important than the actual magnitudes of the individual values, a line graph would have worked better.

Dashboards - solutions



Line graphs make it especially easy to see the patterns of change and to focus on trends. To avoid the clutter of seven lines on a single graph, I used "small multiples," a series of seven small graphs, which vary by region, but otherwise look and work the same. Small multiples may be arranged vertically (shown above), horizontally, or in a matrix. Because this information is a projection (and so the exact magnitudes are probably not as important), I have made the assumption that the graphs should be arranged to make it easiest to compare the patterns of change for the various regions, which is why I aligned the years by arranging the graphs vertically. If the magnitudes of the lines were more important, then a horizontal layout would have been preferable, for easier magnitude comparisons. Notice that the horizontal label (showing the years) is only shown on the very bottom of the graph. This is all that's necessary to show which part of each line belongs to which year. Duplicating these labels for each graph would have resulted in redundancy and clutter.

I have reordered the continents based on the 2006 values, with the highest at the top and the lowest at the bottom. I based the sequence on the 2006 value because, as these values are projections, the first year is likely to be most reliable and of greatest interest to decision-makers.

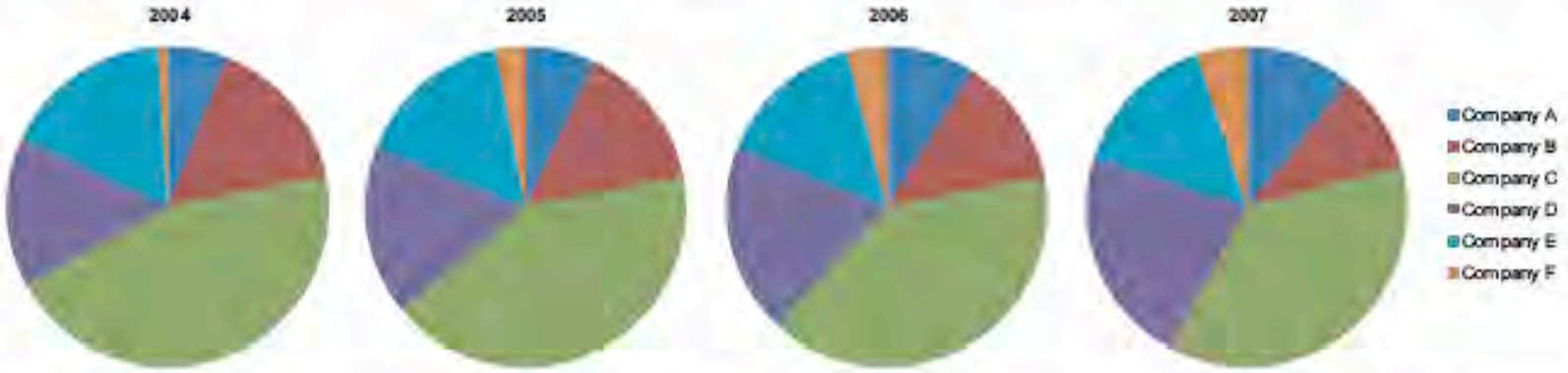
This new design is clean and clear—free of the visual distractions in the first two examples. Anyone viewing the graph would be able to examine the data, focusing perhaps on the large declines that are projected to occur in Europe and Africa, instead of the pretty, shiny bars.

Reduce the non-data ink

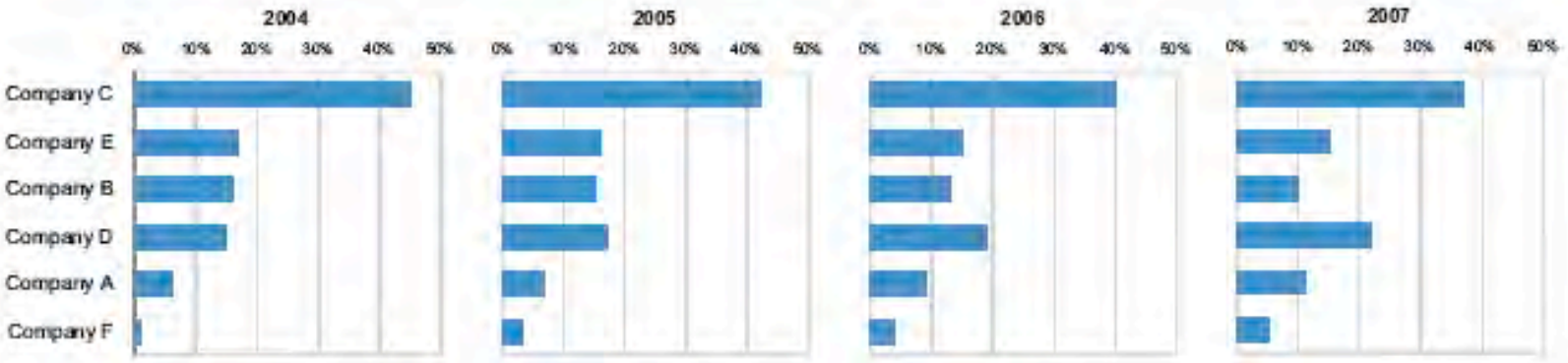
Enhance the data ink

Dashboards - evil pies

Let's examine another ineffective use of pie charts. Edward Tufte once said that "the only worse design than a pie chart is several of them, for then the viewer is asked to compare quantities located in spatial disarray both within and between pies" (Edward Tufte, *The Visual Display of Quantitative Information*, Graphics Press, 1983, p. 178.) I share Tufte's opinion that this is an ineffective way to compare multiple part-to-whole relationships.



Try to follow the changes of these various companies and how they compare to one another through time. It is nearly impossible. Notice how easily you can do it, however, using the following display:



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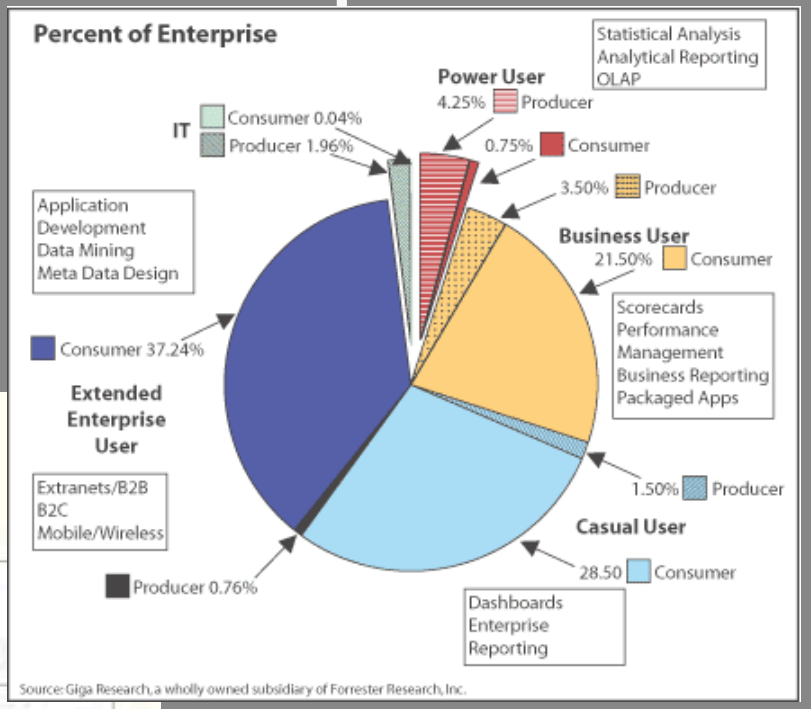
Dashboards - evil pies

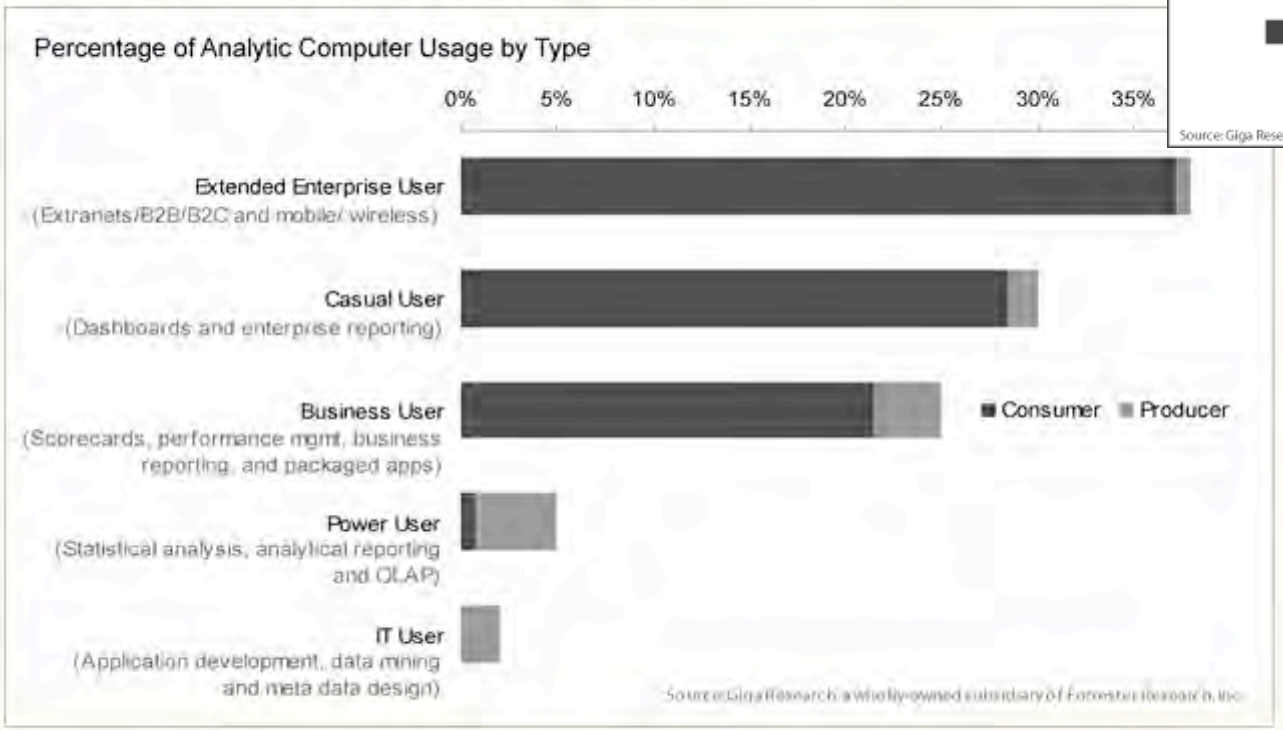


My Analysis

The data is great but the display is a jumbled mess.

A Solution

Here's the same data displayed simply and clearly:



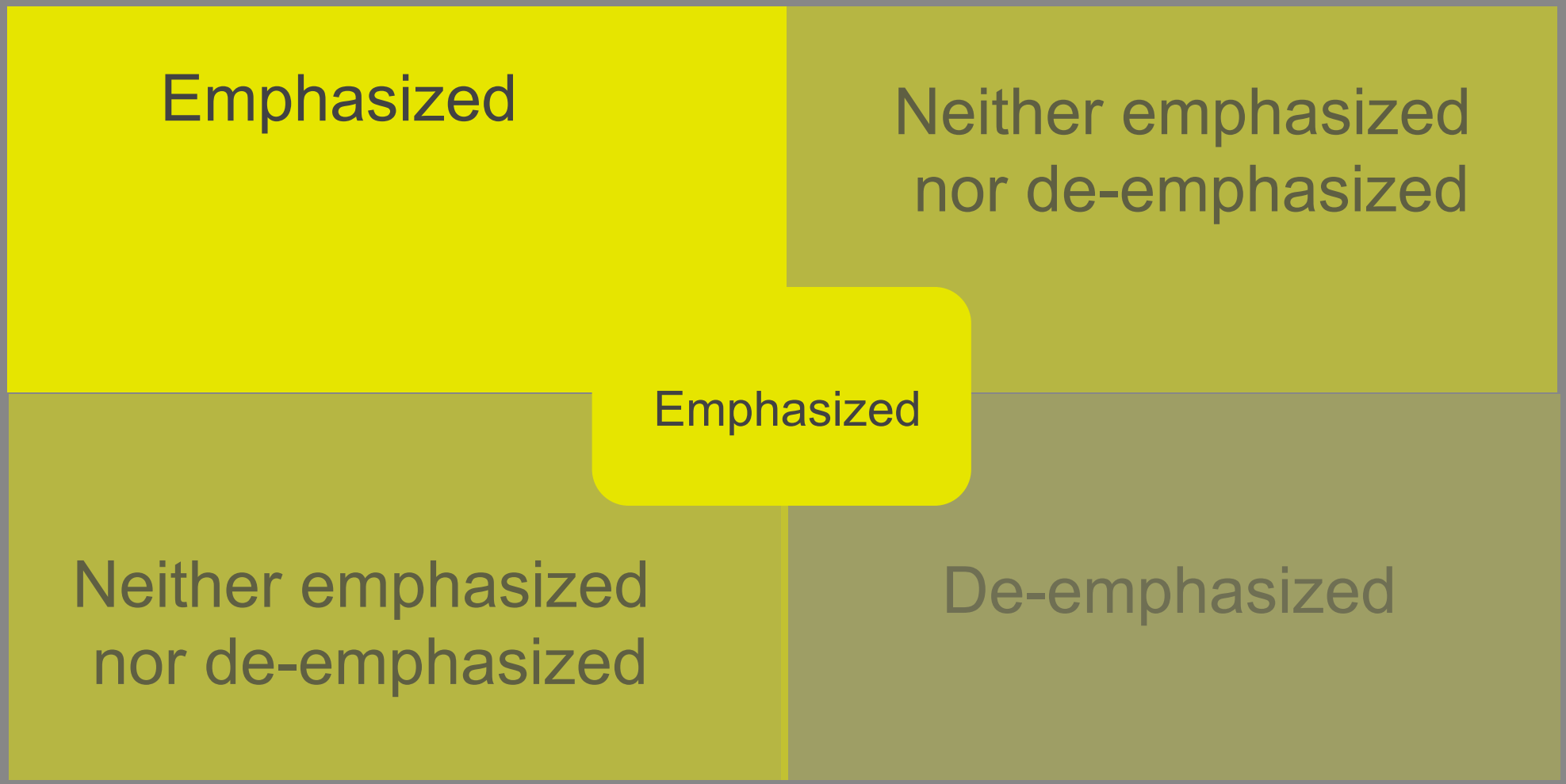
I could have used colors but, frankly, this graph doesn't need them. Limiting it to black and white allows you to photocopy this useful information and pass it on without any loss of quality. Can you imagine what the original pie chart would look like if you photocopied it in black and white?

Reduce the non-data ink

Enhance the data ink

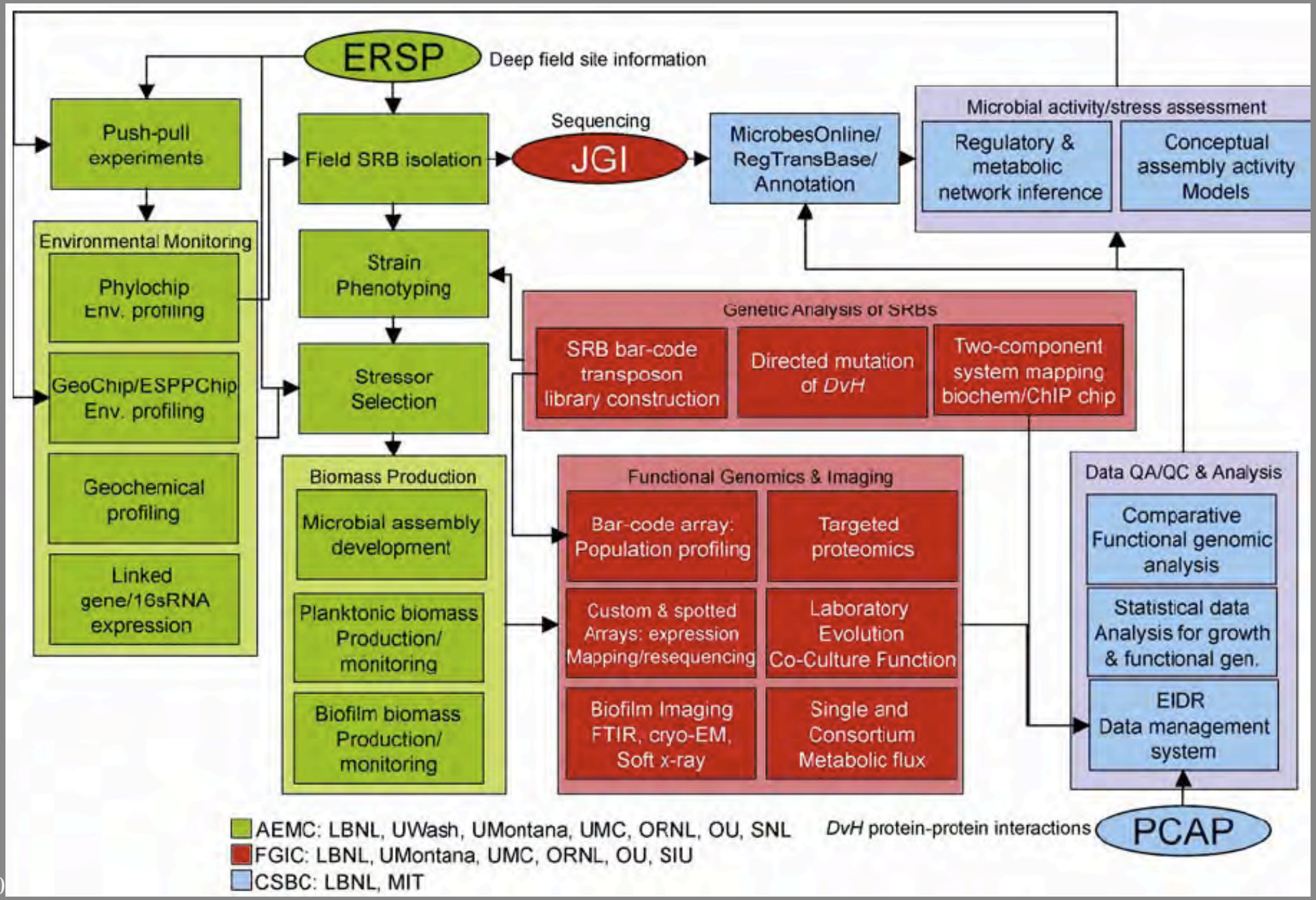
Dashboards - real estate

"The relative prominence of screen space on a dashboard can be divided into quadrants… Whenever possible, place information that is considered most important in the upper left hand region and that which is least important in the lower right hand corner."

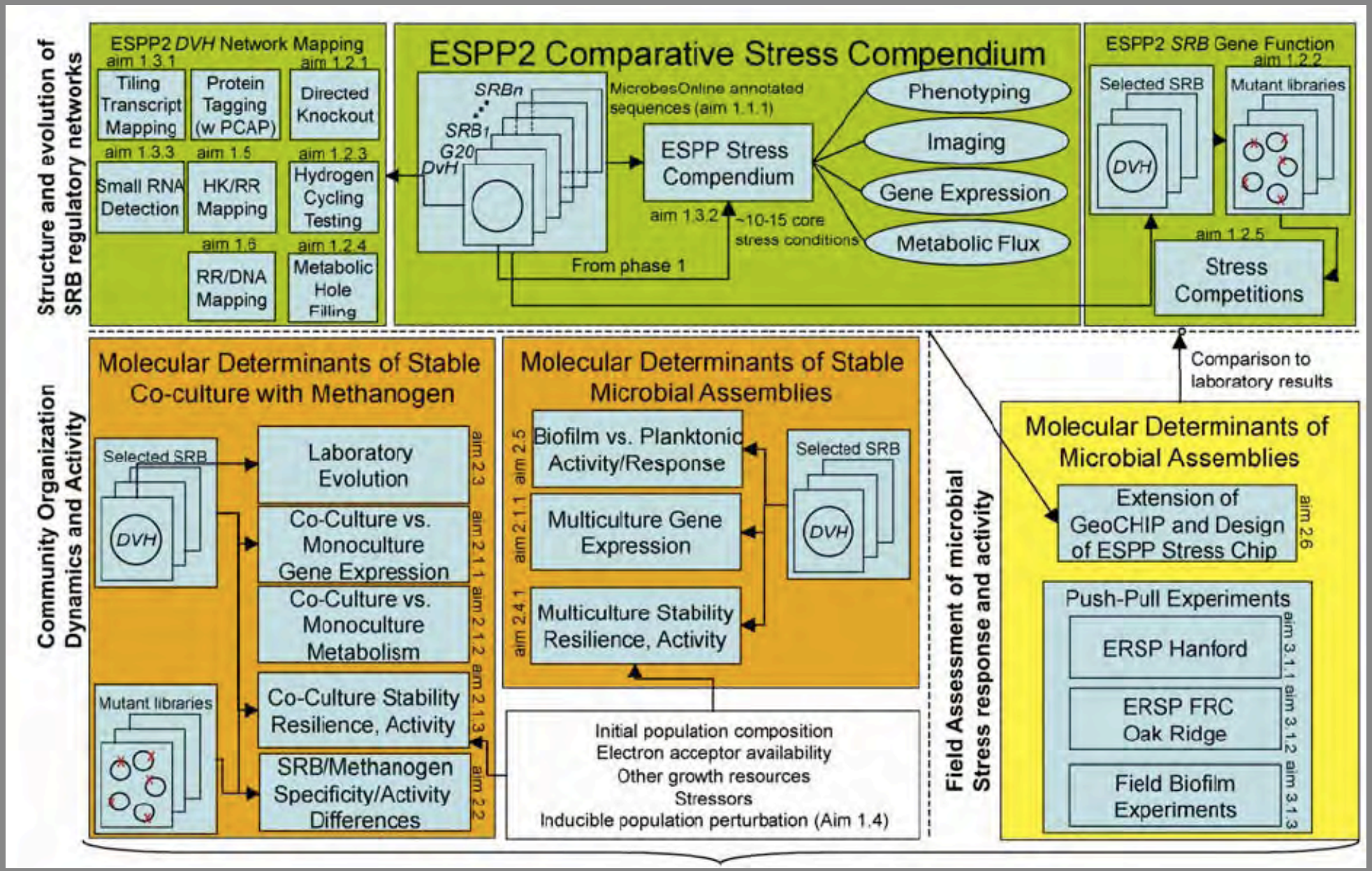


from 'With Dashboards Formatting and Layout Definitely Matter' by Stephen Few

Team Science Approach



Team Science Approach



Milestones: Year One 09/30/2008

AEMC

- Obtain previously isolated SRB (especially for DOE contaminated sites), prepare DNA for sequencing submit to JGI.
- Growth optimization and stability studies of different syntrophic co-culture assemblies: Alternative Dv strains/species.
- Full scale biomass production for steady-state growth stress-perturbed co-culture response experiments (perturbation & steady state analyses using optimized co-culture conditions) for different SRB/methanogen pairs.
- Initial tests of multiculture conditions.
- Initiation of co-culture evolution experiments.
- Optimize transposon strain library competition experiments for read-out by bar code arrays both in monoculture and co -culture.
- Complete membrane profiling of *D. vulgaris* and *M. maripaludis* in mono culture and together in syntrophic culture.
- Design of push-pull experiments and initial characterization of site bacterial populations and geochemistry and Hanford and Oak Ridge, including initial testing of in well sediment/attachment simulation systems.
- Design larger scale attached stress experiments for comparison with planktonic experiments (transcriptomics).
- Complete contrast/compare studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries), 16SRNA Phylochip, Geochip, and realtime Q-PCR.

FGIC

- Create and sequence-verify saturating tagged transposon library of *D. vulgaris* and *D. alaskensis* G20.
- Prioritize HK/RR pair characterization with Computational Core.
- Tag and purify HK/RR pairs.
- Initial HK/RR mapping by biochemical assay.
- Initial proof of concept RR/DNA mapping using ChIP-chip.
- Optimize barcode array design.
- Optimize tiling array for transcription start-stop mapping, small RNA detection and ChIP-chip in SRB for G20 and DvH.
- Optimize multiplex gene expression design for G20.
- Complete stress response transcriptomics for G20.
- Initial survey of possible small RNA regulators.
- Complete design and testing of ESPPChip microarray.

CSBC

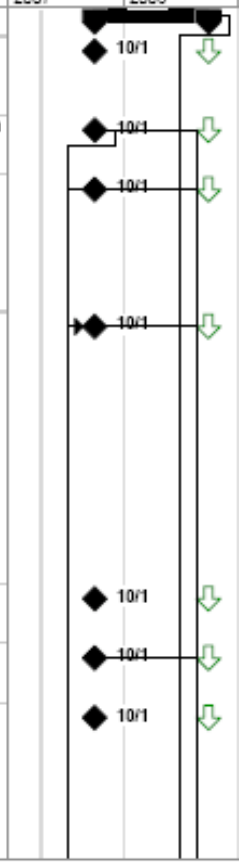
- Extension of MicrobesOnline for 16SRNA, GeoCHIP/ESPPChip, Phenotype, metagenomic data.
- Complete computational analysis of DvH and G20 and methanogen metabolism.
- Establish flux model analysis methods for mono- and multicultures.
- Developing tiling array and bar-code array design and analysis techniques.
- Complete annotation of Dv Miyazaki, Ds 27774, and one Dv Hanford isolate.
- Complete initial reannotation of DvH.
- Begin design of conceptual model of stress, ED, TEA responses for Hanford Cr and Oak Ridge U contaminated sites.

Work Breakdown Structure by Milestones

Schedule Development & Execution

VIMSS/ESPP2 Annual Milestones by Core Groups

ID	WBS	Task Name	Predecessors	Resource Names
1	1	**AEMC Year One**		Terry Hazen
2	1.1	Obtain previously isolated SRB, prepare DNA for sequencing submit to JGI		Terry Hazen
3	1.2	Begin isolation of SRB from ORNL/FRC and Hanford Sites		Matthew Fields,Martin Keller
4	1.3	Growth optimization and stability studies of different syntrophic co-culture assemblies: Alternative Dv strains/species		David Stahl
5	1.4	Full scale biomass production for steady-state growth stress-perturbed co-culture response experiments (perturbation and steady state analyses using optimized co-culture conditions) for different SRB/methanogen pairs.	4SS	Terry Hazen,David Stahl
6	1.5	Initial tests of multi-culture conditions.		David Stahl,Martin Keller,Joe Zhou
7	1.6	Initiation of co-culture evolution experiments.		Kristina Hillesland
8	1.7	Optimize transposon strain library competition experiments for read-out by bar code arrays both in monoculture and co-culture.		Judy Wall,Adam Deutschbauer

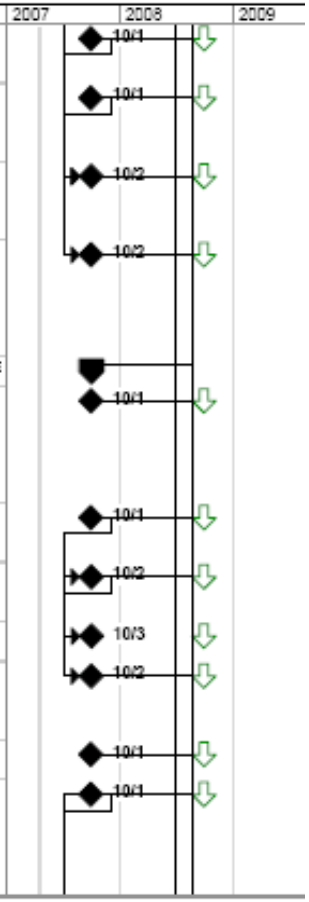


Project: Year 5 Milestones
Date: Tue 4/17/07

Task
Progress
Milestone
Summary
Rolled Up Task
Rolled Up Milestone
Rolled Up Progress
Split

VIMSS/ESPP2 Annual Milestones by Core Groups

ID	WBS	Task Name	Predecessors	Resource Names
9	1.8	Complete membrane profiling of D. vulgaris in mono culture.		Terry Hazen
10	1.9	Complete membrane profiling M. maripaludis in mono culture.		Terry Hazen
11	1.10	Complete membrane profiling of D. vulgaris / M. maripaludis in syntrophic culture.	9,10	David Stahl
12	1.11	Design of push-pull experiments and initial characterization of site bacterial populations and geochemistry.	3	Terry Hazen,Martin Keller,Matthew Fields,Joe Zhou
13	2	**FGIC Year One**		Jay Keasling,Aindrila
14	2.1	Create and sequence-verify saturating tagged transposon library of D. vulgaris and D. alaskensis G20.		Judy Wall
15	2.2	Prioritize HK/RR pair characterization with Computational Core		Aindrila Mukhopadhyay,Adam Deutschbauer
16	2.3	Initial HK/RR mapping by biochemical assay.	15	Aindrila Mukhopadhyay
17	2.4	Tag and purify HK/RR base pairs.	16	Aindrila Mukhopadhyay
18	2.5	Initial proof of concept RR DNA mapping using ChIP chip.	15	Adam Deutschbauer
19	2.6	Optimize barcode array design.		Adam Deutschbauer
20	2.7	Optimize tiling array for transcription start-stop mapping, small RNA detection and ChIP-chip in SRB for G20 and DvH.		Adam Deutschbauer,Kelly Bender



Project: Year 5 Milestones
Date: Tue 4/17/07

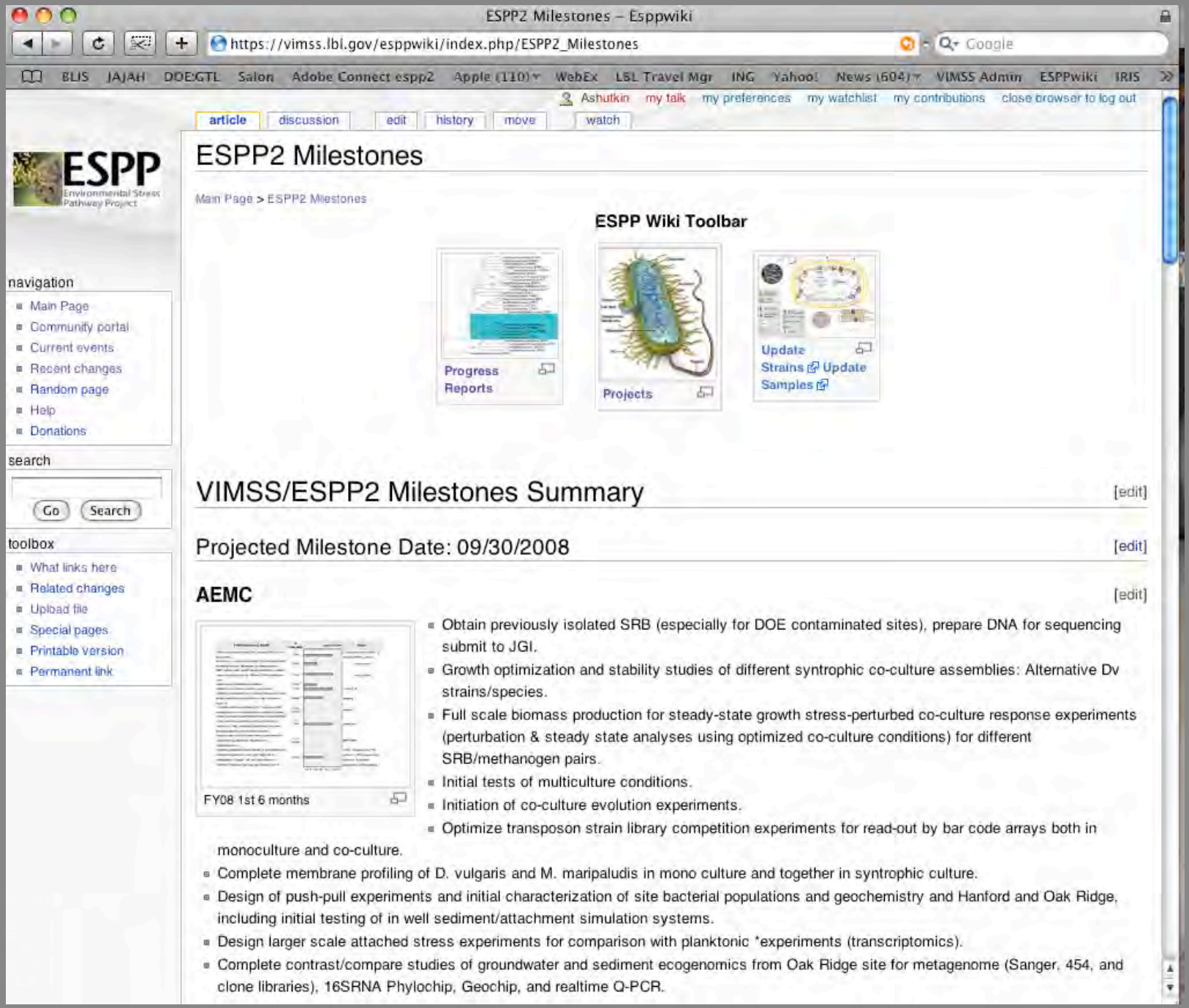
Task
Progress
Milestone
Summary
Rolled Up Task
Rolled Up Milestone
Rolled Up Progress
Split

Dashboard Milestone Reports

FY08 Milestones: AEMC	% Complete	as of 04/01/08	Notes
Obtain previously isolated SRB, prepare DNA for JGI sequencing.	70%		*D. vulgaris Hanford HBLS, D. hanfordii HMW + others*
Syntrophic co-culture assemblies: Growth optimization & stability studies: Alternative Dv strains/species.	30%		*need update*
BMP: steady-state growth stress-perturbed co-culture response experiments for different SRB/methanogen pairs.	70%		*need update*
Initial tests of multiculture conditions.	30%		
Initiation of co-culture evolution experiments.	70%		*U WA & OK*
Optimize monoculture and co-culture transposon strain library competition experiments for bar code array read-out.	50%		*ongoing*
Complete membrane profiling of D. vulgaris and M. maripaludis in mono culture and in syntrophic culture.	*need update*		*Aindrila*
Design push-pull experiments & initial characterization of site bacterial populations and geochemistry @ Hanford & ORNL, including initial testing of in well sediment/attachment simulation systems.	70%		*under way*
Design larger scale attached stress experiments for comparison w/ planktonic *experiments (transcriptomics).	*need update*		*Matt Fields*
Complete contrast/compare studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries), 16SRNA Phylochip, Geochip, and realtime Q-PCR.	50%		*CSBC: Metagenome FRC grdwater - DNA sequencing complete, annotation completed, draft circulating.*
		Oct 07- Mar 08 Apr - Sep 08	

Key Performance Indicators (KPI) ~ essential tasks draw attention to problem areas

Dashboard Milestone Reports



ESPP wiki

Dashboard Milestone Reports

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BMP: steady-state growth stress-perturbed co-culture response experiments for different SRB/methanogen pairs.	70%	*need update*
Initial tests of multiculture conditions.	30%	
Initiation of co-culture evolution experiments.	70%	*U WA & OK*
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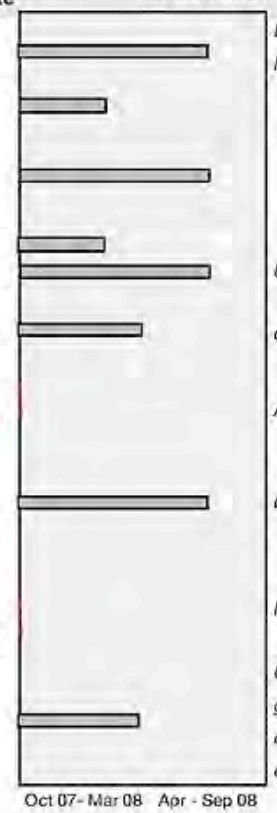


Size of this preview: 776 × 600 pixels

Full resolution (2200 × 1700 pixel, file size: 276 KB, MIME type: image/jpeg)
ESPP2 Milestones > Image:AEMC.jpg > Main Page > ESPP2 Milestones > Image:AEMC.jpg

File history

Legend: (cur) = this is the current file, (del) = delete this old version, (rev) = revert to this old version.
Click on date to see the file uploaded on that date.

- (del) (cur) 20:29, 7 April 2008 . . Ashuffkin (Talk | contribs) . . 2200x1700 (282,122 bytes)

- Upload a new version of this file
- Edit this file using an external application

Cost Estimation & Budget Oversight

Rate Type	FY07	FY08	FY09	FY10	FY11	FY12 (est)	5 Year Totals
Escalation Rates							
LBNL Labor	3.5%	3.0%	3.0%	3.0%			
LBNL Supplies & Other Expenses (OMB)							

Original Project Budget Assumptions

Total Labor	$3,77
Total Supplies & Other Expenses (OMB)	$4,26
Totals	$8,04

Renewal Budget Assumptions

LBNL Labor	
Equipment, Supplies & Other Expenses, LBNL (OMB)	
LBNL Total	
Total Direct Costs, LBNL	
Total Indirect Costs, LBNL	
Total Direct Costs less Other Inst. Indirect Costs, LBNL	
SNL	
ORNL	
ESPP2 Total	
% original projection	

DOE F 4620.1
(04-93)
All Other Editions Are Obsolete

U.S. Department of Energy
Budget Page
(See reverse for Instructions)

ORGANIZATION: Ernest O. Lawrence Berkeley National Laboratory

PRINCIPAL INVESTIGATOR/PROJECT DIRECTOR: Arkin, Adam

Overall Project Budget

A. SENIOR PERSONNEL: PI/PD, Co-PI's, Faculty and Other Senior Associates (List each separately with title; A.6. show number in brackets)	DOE Funded Person-mos. CAL	ACAD	SUMR
1. Arkin, Adam	15.00		
2. Keasling, Jay	6.00		
3. Hazen, Terry	6.00		
4. Dubchak, Inna	18.00		
5.			
6. (6) OTHERS (LIST INDIVIDUALLY ON BUDGET EXPLANATION PAGE)	231.00		
7. (11) TOTAL SENIOR PERSONNEL (1-6)	336.00		
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)			
1. (0) POST DOCTORAL ASSOCIATES	108.00		
2. (25) OTHER PROFESSIONAL (TECHNICIAN, PROGRAMMER, ETC.)	699.00		
3. (2) GRADUATE STUDENTS	54.60		
4. (0) UNDERGRADUATE STUDENTS	0.00		
5. (2) SECRETARIAL - CLERICAL	30.00		
6. (0) OTHER	0.00		
TOTAL SALARIES AND WAGES (A+B)			
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)			
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A+B+C)			
D. PERMANENT EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM.)			
TOTAL PERMANENT EQUIPMENT			
E. TRAVEL 1. DOMESTIC (INCL. CANADA AND U.S. POSSESSIONS)			
2. FOREIGN			
TOTAL TRAVEL			
F. TRAINEE/PARTICIPANT COSTS			
1. STIPENDS (Itemize levels, types + totals on budget justification page)			
2. TUITION & FEES			
3. TRAINEE TRAVEL			
4. OTHER (fully explain on justification page)			
TOTAL PARTICIPANTS (0) TOTAL COST			
G. OTHER DIRECT COSTS			
1. MATERIALS AND SUPPLIES			
2. PUBLICATION COSTS/DOCUMENTATION/DISSEMINATION			
3. CONSULTANT SERVICES			
4. COMPUTER (ADPE) SERVICES			
5. SUBCONTRACTS			
6. OTHER			
TOTAL OTHER DIRECT COSTS			
H. TOTAL DIRECT COSTS (A THROUGH G)			
I. INDIRECT COSTS (SPECIFY RATE AND BASE) *Please see the indirect calculation sheets*			
TOTAL INDIRECT COSTS			
J. TOTAL DIRECT AND INDIRECT COSTS (H+I)			
K. AMOUNT OF ANY REQUIRED COST SHARING FROM NON-FEDERAL SOURCES			
L. TOTAL COST OF PROJECT (J+K)			

LBNL Forward Pricing Rates
Effective October 1, 2006
Revision 5

Rate Type

Escalation Rates
- Labor
- Supplies & Other Expenses (OMB)
- Construction Projects (OECM)

Institutional Rates

General and Administrative
- G&A (Off Site) Rate - OFF
- Site Support (Fabrication) Rate - FAB
  - Gretina
  - Animal Care
- General Rate - GR1

LDRD Rate
- LDRD Operating and Equipment
- (LDRD rate is based on proposed structure, which is currently being reviewed by DOE)

IGPP Rate
- IGPP

Procurement Burdens (Base: Cost of procured materials & services)
- PO's $1-$500,000
- PO's Over $500,000 (per PO) $
- R&D subcontract's $1-$300,000
- R&D subcontract's over $300,000 $
- Intra-University Transfers (IUTs) $1-$200,000
- Intra-University Transfers (IUTs) over $200,000
- Genomics Procurements (PO's $1-$500,000)
- Molecular Foundry (PO's $1-$500,000)
- Project Management (PO's $1-$500,000)

Travel (Base: Travel Costs)
- Travel Rate

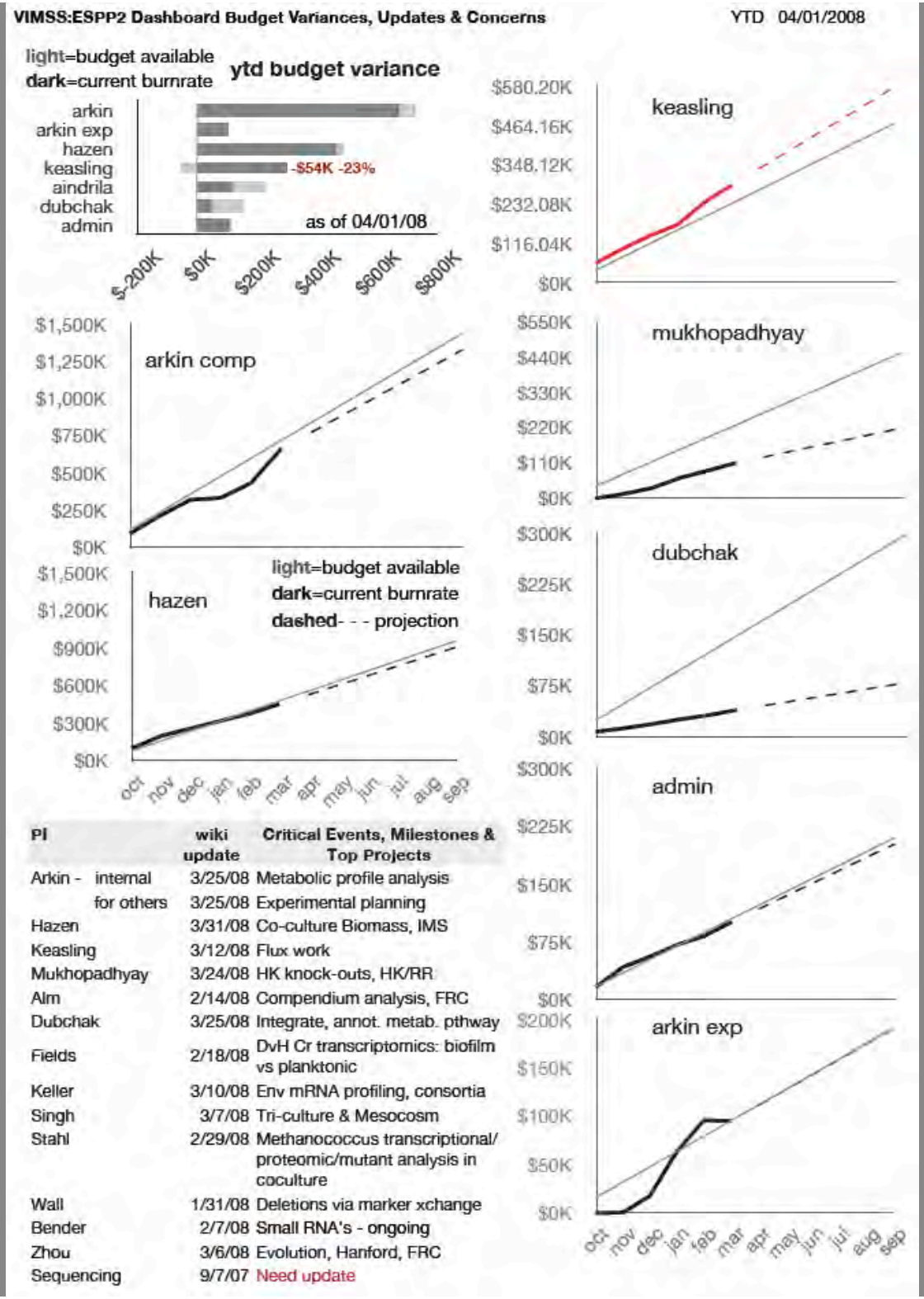
Payroll Burden (Base: Delivered effort cost only)
- **Career&Term Employees**
- Post Docs, Visiting Post Docs, Limited Employees, and Visting Researchers
- GSRAs
- Students/Rehired Retirees/Employees working variable time
- Summer Faculty

Fringe Benefits Only (Base: FTE gross pay only)
- **Career&Term Employees**
- Post Docs, Visiting Post Docs, Limited Employees, and Visting Researchers
- GSRAs
- Students/Rehired Retirees/Employees working variable time
- Summer Faculty

ESPP2 Environmental Stress Pathway Project

Dashboard Integrated Milestone & Budget Reports

"How then do we make it easy for people to compare related sets of values when they are associated with different units of measure? Two answers come to mind. The first and most obvious is to place them in separate graphs, positioned close to one another so that the patterns in each can be compared to one another, but magnitude comparisons will be discouraged." *Stephen Few*



PI	wiki update	Critical Events, Milestones & Top Projects
Arkin - internal	3/25/08	Metabolic profile analysis
for others	3/25/08	Experimental planning
Hazen	3/31/08	Co-culture Biomass, IMS
Keasling	3/12/08	Flux work
Mukhopadhyay	3/24/08	HK knock-outs, HK/RR
Alm	2/14/08	Compendium analysis, FRC
Dubchak	3/25/08	Integrate, annot. metab. pthway
Fields	2/18/08	DvH Cr transcriptomics: biofilm vs planktonic
Keller	3/10/08	Env mRNA profiling, consortia
Singh	3/7/08	Tri-culture & Mesocosm
Stahl	2/29/08	Methanococcus transcriptional/ proteomic/mutant analysis in coculture
Wall	1/31/08	Deletions via marker xchange
Bender	2/7/08	Small RNA's - ongoing
Zhou	3/6/08	Evolution, Hanford, FRC
Sequencing	9/7/07	Need update

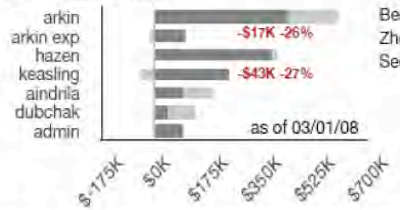
Dashboard Integrated Milestone & Budget Reports

FY08 Milestones: CSBC	% Complete	as of 04/01/08	Notes
Extension of MicrobesOnline for:			
16SRNA	50%		
GeoCHIP/ESPPChip	0%		*working w/ ORNL to incorporate Selexa data*
Phenotype	50%		*usefulness will depend on human (undergrads) annotation*
Metagenomic data	25%		
Complete computational analysis of DvH & G20 + methanogen metabolism.	50%		*Waiting on data.*
Establish flux model analysis methods for mono- and multicultures.	50%		*High potential value & high interest*
Developing tiling array and bar-code array design and analysis techniques.	90%		*Analysis techniques will continue to evolve & improve*
Complete annotation of Dv Miyazaki, Ds 27774, and one Dv Hanford isolate.	50%		*Waiting for these + other sequences before expression array & analysis*
Complete initial reannotation of DvH.	50%		*Additional data to include? Tiling array?*
Begin design of conceptual model of stress, ED, TEA responses for Hanford Cr and Oak Ridge U contaminated sites.	0%		*Participating in experimental design - conceptual model depends on data to be collected*

Oct 07- Mar 08 Apr - Sep 08

light=budget available
dark=current burnrate

ytd budget variance



PI	wiki update	Critical Events, Milestones & Top Projects
Arkin - internal	3/7/08	Microarray analysis
for others	3/11/08	Metabolomics condition set
Hazen	3/14/08	Co-culture Biomass, IMS
Keasling	3/12/08	Tryptophan biosynthesis
Mukhopadhyay	3/12/08	HK knock-outs, HK/RR
Alm	2/14/08	Compendium analysis, FRC
Dubchak	1/31/08	Hiring Pavel
Fields	2/18/08	DvH Cr transcriptomics: biofilm vs planktonic
Keller	2/7/08	Consortia culture
Singh	3/7/08	Tri-culture & Mesocosm
Stahl	2/29/08	Methanococcus transcriptional/proteomic/ mutant analysis in coculture
Wall	1/31/08	Deletions via marker xchange
Bender	2/6/08	Small RNA's
Zhou	3/6/08	Evolution, Hanford, FRC
Sequencing	9/7/07	Need update

FY08 Milestones: FGIC	% Complete	as of 04/01/08	Notes
Create and sequence-verify saturating tagged transposon libraries for:			*Adam D.*
D. vulgaris	10%%		*just started*
D. alaskensis G20	50%		*100% created, sequence verification ongoing*
Prioritize HK/RR pair characterization w/ CSBC.	30%		
Tag and purify HK/RR pairs.	70%		*RR - 90%, HK - 50%*
Initial HK/RR mapping by biochemical assay.	50%		*Post-doc to begin 08/01. All HK knock-outs: 12/64 genes completed, 2-3 checked. Paper in process.*
Initial proof of concept RR/DNA mapping using ChIP-chip.	50%		*Ready to go - waiting on Nimblegen chips (Adam D. & Paramvir)*
Optimize barcode array design.	50%		*(Adam D. & Paramvir)*
Optimize tiling array for transcription start-stop mapping, small RNA detection and ChIP-chip in SRB for G20 and DvH.	0%		*Will need to recast into year 2 milestones.*
Optimize multiplex gene expression design for G20.	need update		*Adam D.*
Complete stress response transcriptomics for G20.	need update		*Adam D.*
Initial survey of possible small RNA regulators.	30%		*Kelly Bender - 1 study complete*
Complete ESPPChip microarray design & testing.	need update		*Redundant? Combine w/ Chip-chip development?*
Gene expression compendium	need update		
Metabolomics	need update		

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FY08 Milestones: AEMC	% Complete	as of 04/01/08	Notes
Obtain previously isolated SRB, prepare DNA for JGI sequencing.	70%		*D. vulgaris Hanford HBLS, D. hanfordii HMW + others*
Syntrophic co-culture assemblies: Growth optimization & stability studies: Alternative Dv strains/species.	30%		*need update*
BMP: steady-state growth stress-perturbed co-culture response experiments for different SRB/methanogen pairs.	70%		*need update*
Initial tests of multiculture conditions.	30%		
Initiation of co-culture evolution experiments.	70%		*U WA & OK*
Optimize monoculture and co-culture transposon strain library competition experiments for bar code array read-out.	50%		*ongoing*
Complete membrane profiling of D. vulgaris and M. maripaludis in mono culture and in syntrophic culture.	need update		*Aindrila*
Design push-pull experiments & initial characterization of site bacterial populations and geochemistry @ Hanford & ORNL, including initial testing of in well sediment/attachment simulation systems.	70%		*under way*
Design larger scale attached stress experiments for comparison w/ planktonic *experiments (transcriptomics).	need update		*Matt Fields*
Complete contrast/compare studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries), 16SRNA Phylochip, Geochip, and realtime Q-PCR.	50%		*CSBC: Metagenome FRC grdwater - DNA sequencing complete, annotation completed, draft circulating.*

Oct 07- Mar 08 Apr - Sep 08

Acknowledgements

http://vimss.lbl.gov

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- **Montana State University**, Matthew Fields

Functional Genomics and Imaging Core:

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- **University of Missouri-Columbia**, Judy Wall
- **Southern Illinois University**, Kelly Bender
- **Sandia National Laboratory**, Anup Singh
- **Oak Ridge National Laboratory**, Martin Keller
- **University of Oklahoma**, Jizhong (Joe) Zhou

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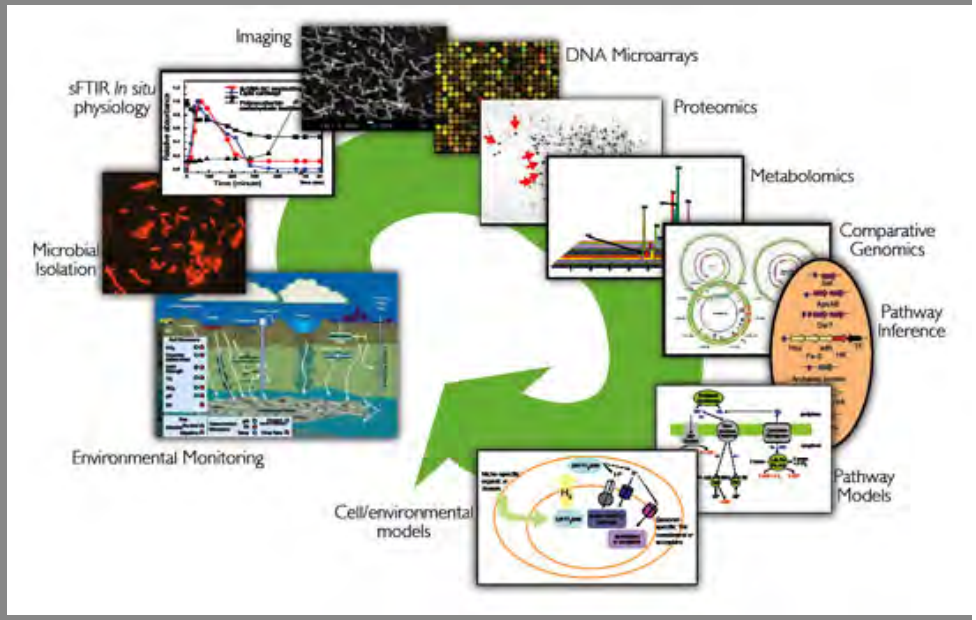
- **LBNL**: Adam P. Arkin, Inna Dubchak, Paramvir Dehal
- **MIT**: Eric Alm



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